

```

OTHER INFORMATION: Incyte ID No: 054316CB1
US-09-974-298-126

Query Match      100.0%; Score 509; DB 41; Length 509;
Rest Local Similarity 100.0%; Pred. No. 2e-124;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTGAGAGGAGTGAAGGATCGCGTTCCTGCTGCTGAGACTTTTCTGTCACATGAA 60
DB 1 GAGTTGAGAGGAGTGAAGGATCGCGTTCCTGCTGCTGAGACTTTTCTGTCACATGAA 60
QY 61 CGAGAGCTGTGTAATATGATTTGGGAGAGAGATCAATATAGGCTTAGGCCAGAGAG 120
DB 61 CGAGAGCTGTGTAATATGATTTGGGAGAGAGATCAATATAGGCTTAGGCCAGAGAG 120
QY 121 AAGGTACACCTCTCTGAGCTGATTGGGCTTAGCTGAGCCCGGTGATGAGAGCTTCA 180
DB 121 AAGGTACACCTCTCTGAGCTGATTGGGCTTAGCTGAGCCCGGTGATGAGAGCTTCA 180
QY 181 GCAAGAGAAACCAACCACTTAAGTGGGATCTCTGACCTGCTCAGAGAGAGAGAGAA 240
DB 181 GCAAGAGAAACCAACCACTTAAGTGGGATCTCTGACCTGCTCAGAGAGAGAGAGAA 240
QY 241 TCAGGGGAGCTGAGACTTAAGTGGGCTGACCTGAGAGCTGATCTCAGAGAGCTGTCA 300
DB 241 TCAGGGGAGAGCTGAGACTTAAGTGGGCTGACCTGAGAGCTGATCTCAGAGAGCTGTCA 300
QY 301 GTCAAGACTGGGGGAGTAATGTGAAAATGGTCTGTGACCAAGGGAGAGATTCTGCCAA 360
DB 301 GTCAAGACTGGGGGAGTAATGTGAAAATGGTCTGTGACCAAGGGAGAGATTCTGCCAA 360
QY 361 ATCAGAACATTTAAATATGCGAGAGAGAGTGAACGCAACACAGCTTTAAATGAAGAC 420
DB 361 ATCAGAACATTTAAATATGCGAGAGAGAGTGAACGCAACACAGCTTTAAATGAAGAC 420
QY 421 AAGCTGAACAACAACAAACGTTTATATCTAAGATTTGACTTAAATAATCAATA 480
DB 421 AAGCTGAACAACAACAAACGTTTATATCTAAGATTTGACTTAAATAATCAATA 480
QY 481 AACTTTGAGCTTCTCCAAAAA 509
DB 481 AACTTTGAGCTTCTCCAAAAA 509

```

FILE REFERENCE: PB-0016 US

```

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO: 7
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 257708
US-09-996-952-7

Query March 100.0% Score 509; DB 42; Length 509;
Best Local Similarity 100.0%; Pred No. 2e-124;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTGTGAAGGAGTGTGAAGGTCGCCCTCTGCTGTCTGTGAATTTTTCGTCACATGTACA 60
Db 1 GAGTTGTGAAGGAGTGTGAAGGTCGCCCTCTGCTGTCTGTGTGAATTTTTCGTCACATGTACA 60

```

QY 61 CGAGCTGTGTAATATGATTGGCGAGAGATCAATATAGGCTTAGGCGAGAG 120
DB 61 CGAGCTGTGTAATATGATTGGCGAGAGATCAATATAGGCTTAGGCGAGAG 120
QY 121 AAGGTGACCACTCTCTAGCTGATTGGGCTTACTGTGAGCCCGGTATGAGAGCTCA 180
DB 121 AAGGTGACCACTCTCTAGCTGATTGGGCTTACTGTGAGCCCGGTATGAGAGCTCA 180
QY 181 GCAAGAGAACCAACCACTGAAAGTCCGGAATCTGTGACCTGTGACGAGAGAGAGAGA 240
DB 181 GCAAGAGAACCAACCACTGAAAGTCCGGAATCTGTGACCTGTGACGAGAGAGAGA 240
QY 241 TCAGGGTGCAGCTGAGACTCAAGTCTGACCTGAGAGAGTGTCTCAAGAGCTGTCTCA 300
DB 241 TCAGGGTGCAGCTGAGACTCAAGTCTGACCTGAGAGAGTGTCTCAAGAGCTGTCTCA 300
QY 301 GTCAAAAGACTGGGGGTGAATGTGAAATGCTGATGACAGAGGAGAGATCTGCGCAA 360
DB 301 GTCAAAAGACTGGGGGTGAATGTGAAATGCTGATGACAGAGGAGAGATCTGCGCAA 360
QY 361 ATCGAACAATTAAATATGCCAGAGAGGTGACAGGCAACAAGTTTAAATGAAGAC 420
DB 361 ATCGAACAATTAAATATGCCAGAGAGGTGACAGGCAACAAGTTTAAATGAAGAC 420
QY 421 AAGCTGAAACAACAACAACTGTTTATCTAAGATATTTGACTTAAATATCAATAA 480
DB 421 AAGCTGAAACAACAACAACTGTTTATCTAAGATATTTGACTTAAATATCAATAA 480
QY 481 AACTTTGACAGCTTTCTCCAAAAA 509
DB 481 AACTTTGACAGCTTTCTCCAAAAA 509

RESULT 3

US-10-051-835-11
Sequence 11, Application US/10051835
GENERAL INFORMATION:
APPLICANT: Jones, Amy W.
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS
FILE REFERENCE: PA-0044 US
CURRENT APPLICATION NUMBER: US/10/051,835
CURRENT FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 064516CB1
US-10-051-835-11

Query Match 100.0%; Score 509; DB 44; Length 509;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTGTAGGGGTGAGGGTGGCTTCCCTGCTGCTGAGACTTTTCTGTCCACTGAGA 60
DB 1 GAGTTGTAGGGGTGAGGGTGGCTTCCCTGCTGCTGAGACTTTTCTGTCCACTGAGA 60
QY 61 CGAGCTGTGTAATATGATTGGCGAGAGATCAATATAGGCTTAGGCGAGAG 120
DB 61 CGAGCTGTGTAATATGATTGGCGAGAGATCAATATAGGCTTAGGCGAGAG 120
QY 121 AAGGTGACCACTCTCTAGCTGATTGGGCTTACTGTGAGCCCGGTATGAGAGCTCA 180
DB 121 AAGGTGACCACTCTCTAGCTGATTGGGCTTACTGTGAGCCCGGTATGAGAGCTCA 180
QY 181 GCAAGAGAACCAACCACTGAAAGTCCGGAATCTGTGACCTGTGACGAGAGAGAGA 240
DB 181 GCAAGAGAACCAACCACTGAAAGTCCGGAATCTGTGACCTGTGACGAGAGAGAGA 240

QY 241 TCAGGGTGCAGCTGAGACTCAAGTCTGAGAGAGTGTCTGATGACAGAGGAGAGCTCA 300
DB 241 TCAGGGTGCAGCTGAGACTCAAGTCTGAGAGAGTGTCTGATGACAGAGGAGAGCTCA 300
QY 301 GTCAAAAGACTGGGGGTGAATGTGAAATGCTGATGACAGAGGAGAGATCTGCGCAA 360
DB 301 GTCAAAAGACTGGGGGTGAATGTGAAATGCTGATGACAGAGGAGAGATCTGCGCAA 360
QY 361 ATCGAACAATTAAATATGCCAGAGAGGTGACAGGCAACAAGTTTAAATGAAGAC 420
DB 361 ATCGAACAATTAAATATGCCAGAGAGGTGACAGGCAACAAGTTTAAATGAAGAC 420
QY 421 AAGCTGAAACAACAACAACTGTTTATCTAAGATATTTGACTTAAATATCAATAA 480
DB 421 AAGCTGAAACAACAACAACTGTTTATCTAAGATATTTGACTTAAATATCAATAA 480
QY 481 AACTTTGACAGCTTTCTCCAAAAA 509
DB 481 AACTTTGACAGCTTTCTCCAAAAA 509

RESULT 4

US-10-093-766-35
Sequence 35, Application US/10093766
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
APPLICANT: Karpf, Adam R.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REFERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 35
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 064516CB1
US-10-093-766-35

Query Match 100.0%; Score 509; DB 44; Length 509;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTGTAGGGGTGAGGGTGGCTTCCCTGCTGCTGAGACTTTTCTGTCCACTGAGA 60
DB 1 GAGTTGTAGGGGTGAGGGTGGCTTCCCTGCTGCTGAGACTTTTCTGTCCACTGAGA 60
QY 61 CGAGCTGTGTAATATGATTGGCGAGAGATCAATATAGGCTTAGGCGAGAG 120
DB 61 CGAGCTGTGTAATATGATTGGCGAGAGATCAATATAGGCTTAGGCGAGAG 120
QY 121 AAGGTGACCACTCTCTAGCTGATTGGGCTTACTGTGAGCCCGGTATGAGAGCTCA 180
DB 121 AAGGTGACCACTCTCTAGCTGATTGGGCTTACTGTGAGCCCGGTATGAGAGCTCA 180
QY 181 GCAAGAGAACCAACCACTGAAAGTCCGGAATCTGTGACCTGTGACGAGAGAGAGA 240
DB 181 GCAAGAGAACCAACCACTGAAAGTCCGGAATCTGTGACCTGTGACGAGAGAGAGA 240
QY 241 TCAGGGTGCAGCTGAGACTCAAGTCTGACCTGAGAGAGTGTCTCAAGAGCTGTCTCA 300
DB 241 TCAGGGTGCAGCTGAGACTCAAGTCTGACCTGAGAGAGTGTCTCAAGAGCTGTCTCA 300
QY 301 GTCAAAAGACTGGGGGTGAATGTGAAATGCTGATGACAGAGGAGAGATCTGCGCAA 360
DB 301 GTCAAAAGACTGGGGGTGAATGTGAAATGCTGATGACAGAGGAGAGATCTGCGCAA 360
QY 361 ATCGAACAATTAAATATGCCAGAGAGGTGACAGGCAACAAGTTTAAATGAAGAC 420

```

; SOFTWARE: FALCON Program
; SEQ ID NO: 426
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

```

1 GAGTTGTGAGGGTGTGAGGGTCGCCGTTCCCTGCTGTCTGGACTTTTCTCTGTCCCACTGAGA 60

QY 61 CGCAGCTGTGTGAATATGATTTGGCGAGAGATCAATATAGAGCCCTAGGCGAGAG 120
 DB 61 CGCAGCTGTGTGAATATGATTTGGCGAGAGATCAATATAGAGCCCTAGGCGAGAG 120
 QY 121 AAGTGTACCACTCTGAGCTGATTTGGGCTTAATGCTGAGCCCGGTGATGAGAGCTCA 180
 DB 121 AAGTGTACCACTCTGAGCTGATTTGGGCTTAATGCTGAGCCCGGTGATGAGAGCTCA 180
 QY 181 GGAAGAGGAACCAACCACTGAAAGTGGGATCTGCACTGCTGAGGAGAGAGAGAGA 240
 DB 181 GGAAGAGGAACCAACCACTGAAAGTGGGATCTGCACTGCTGAGGAGAGAGAGAGA 240
 QY 241 TCAGGGTGCAGCTGAGACTCAAGTGCCTGAGCTGAGAGCTGATCTCCAGAGCTGTCA 300
 DB 241 TCAGGGTGCAGCTGAGACTCAAGTGCCTGAGCTGAGAGCTGATCTCCAGAGCTGTCA 300
 QY 301 GTCAAGACTGGGGGTGAATGTGGAATGTGCTGATGACCAAGGAGAGATTTGCGCAA 360
 DB 301 GTCAAGACTGGGGGTGAATGTGGAATGTGCTGATGACCAAGGAGAGATTTGCGCAA 360
 QY 361 ATCAGAACATTTAAATGCGAAGAGAGTGAACGCAACCAAGTTTAAATGAGAGC 420
 DB 361 ATCAGAACATTTAAATGCGAAGAGAGTGAACGCAACCAAGTTTAAATGAGAGC 420
 QY 421 AAGCTGAACACACAAACTGTTTATCTAAGATTTGCTTAAATATCAAAATA 480
 DB 421 AAGCTGAACACACAAACTGTTTATCTAAGATTTGCTTAAATATCAAAATA 480
 QY 481 AACTTTGAGCTTTCTCCAAAAAAA 509
 DB 481 AACTTTGAGCTTTCTCCAAAAAAA 509

RESULT 3

US-10-051-835-11
 Sequence 11, Application US/10051835
 GENERAL INFORMATION:
 APPLICANT: Jones, David A.
 APPLICANT: Lasek, Amy W.
 TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS
 FILE REFERENCE: PA-0044 US
 CURRENT APPLICATION NUMBER: US/10/051,835
 CURRENT FILING DATE: 2002-01-16
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PERL Program
 SEQ ID NO 11
 LENGTH: 509
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 064516CB1
 US-10-051-835-11

Query Match 100.0%; Score 509; DB 44; Length 509;
 Best Local Similarity 100.0%; Pred. No. 2e-124;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTGTAGGGGTGTGAGGGTGGCGTTCTGCTGTGAGACTTTTCTGTCCTCACTGAGA 60
 DB 1 GAGTTGTAGGGGTGTGAGGGTGGCGTTCTGCTGTGAGACTTTTCTGTCCTCACTGAGA 60
 QY 61 CGCAGCTGTGTGAATATGATTTGGCGAGAGATCAATATAGAGCCCTAGGCGAGAG 120
 DB 61 CGCAGCTGTGTGAATATGATTTGGCGAGAGATCAATATAGAGCCCTAGGCGAGAG 120
 QY 121 AAGTGTACCACTCTGAGCTGATTTGGGCTTAATGCTGAGCCCGGTGATGAGAGCTCA 180
 DB 121 AAGTGTACCACTCTGAGCTGATTTGGGCTTAATGCTGAGCCCGGTGATGAGAGCTCA 180
 QY 181 GGAAGAGGAACCAACCACTGAAAGTGGGATCTGCACTGCTGAGGAGAGAGAGA 240
 DB 181 GGAAGAGGAACCAACCACTGAAAGTGGGATCTGCACTGCTGAGGAGAGAGAGA 240

QY 241 TCAGGGTGCAGCTGAGACTCAAGTGCCTGAGCTGAGAGCTGATCTCCAGAGCTGTCA 300
 DB 241 TCAGGGTGCAGCTGAGACTCAAGTGCCTGAGCTGAGAGCTGATCTCCAGAGCTGTCA 300
 QY 301 GTCAAGACTGGGGGTGAATGTGGAATGTGCTGATGACCAAGGAGAGATTTGCGCAA 360
 DB 301 GTCAAGACTGGGGGTGAATGTGGAATGTGCTGATGACCAAGGAGAGATTTGCGCAA 360
 QY 361 ATCAGAACATTTAAATGCGAAGAGAGTGAACGCAACCAAGTTTAAATGAGAGC 420
 DB 361 ATCAGAACATTTAAATGCGAAGAGAGTGAACGCAACCAAGTTTAAATGAGAGC 420
 QY 421 AAGCTGAACACACAAACTGTTTATCTAAGATTTGCTTAAATATCAAAATA 480
 DB 421 AAGCTGAACACACAAACTGTTTATCTAAGATTTGCTTAAATATCAAAATA 480
 QY 481 AACTTTGAGCTTTCTCCAAAAAAA 509
 DB 481 AACTTTGAGCTTTCTCCAAAAAAA 509

RESULT 4

US-10-093-766-35
 Sequence 35, Application US/10093766
 GENERAL INFORMATION:
 APPLICANT: Lasek, Amy W.
 APPLICANT: Jones, David A.
 TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
 FILE REFERENCE: PA-0047 US
 CURRENT APPLICATION NUMBER: US/10/093,766
 CURRENT FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: PERL Program
 SEQ ID NO 35
 LENGTH: 509
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 064516CB1
 US-10-093-766-35

Query Match 100.0%; Score 509; DB 44; Length 509;
 Best Local Similarity 100.0%; Pred. No. 2e-124;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTGTAGGGGTGTGAGGGTGGCGTTCTGCTGTGAGACTTTTCTGTCCTCACTGAGA 60
 DB 1 GAGTTGTAGGGGTGTGAGGGTGGCGTTCTGCTGTGAGACTTTTCTGTCCTCACTGAGA 60
 QY 61 CGCAGCTGTGTGAATATGATTTGGCGAGAGATCAATATAGAGCCCTAGGCGAGAG 120
 DB 61 CGCAGCTGTGTGAATATGATTTGGCGAGAGATCAATATAGAGCCCTAGGCGAGAG 120
 QY 121 AAGTGTACCACTCTGAGCTGATTTGGGCTTAATGCTGAGCCCGGTGATGAGAGCTCA 180
 DB 121 AAGTGTACCACTCTGAGCTGATTTGGGCTTAATGCTGAGCCCGGTGATGAGAGCTCA 180
 QY 181 GGAAGAGGAACCAACCACTGAAAGTGGGATCTGCACTGCTGAGGAGAGAGAGA 240
 DB 181 GGAAGAGGAACCAACCACTGAAAGTGGGATCTGCACTGCTGAGGAGAGAGAGA 240
 QY 241 TCAGGGTGCAGCTGAGACTCAAGTGCCTGAGCTGAGAGCTGATCTCCAGAGCTGTCA 300
 DB 241 TCAGGGTGCAGCTGAGACTCAAGTGCCTGAGCTGAGAGCTGATCTCCAGAGCTGTCA 300
 QY 301 GTCAAGACTGGGGGTGAATGTGGAATGTGCTGATGACCAAGGAGAGATTTGCGCAA 360
 DB 301 GTCAAGACTGGGGGTGAATGTGGAATGTGCTGATGACCAAGGAGAGATTTGCGCAA 360
 QY 361 ATCAGAACATTTAAATGCGAAGAGAGTGAACGCAACCAAGTTTAAATGAGAGC 480

PL
NAM

Wed Apr 28 09:27:43 2004

us-10-051-835-11-mpm

Sequence Alignment between
SEQ ID NO: 11 of 10/051,835 and
SEQ ID NO: 35 of 10/093,766
Page 1 of 2

61 CGCAGGCTGTGAAATATGATTTGGCGAGGAGATCAATATAGGCTTACGAGAG 120
Db CGCAGGCTGTGAAATATGATTTGGCGAGGAGATCAATATAGGCTTACGAGAG 120
Qy 121 AAGGTACCACTCTGAGCTGATTTGGGCTATATGCTGAGAGCCCGGTATGAGAGCCCA 180
Db 121 AAGGTACCACTCTGAGCTGATTTGGGCTATATGCTGAGAGCCCGGTATGAGAGCCCA 180
Qy 181 GCAAGAGAACCACTGTAAGTGGAGTCTGCACTGCTGCTGAGAGAGAGAGAGAG 240
Db 181 GCAAGAGAACCACTGTAAGTGGAGTCTGCACTGCTGCTGAGAGAGAGAGAGAG 240
Qy 241 TCAGGGGTGAGCTGAGCTCAATGCTGCTGAGAGAGTATCTCCAGAGAGCTGTCA 300
Db 241 TCAGGGGTGAGCTGAGCTCAATGCTGCTGAGAGAGTATCTCCAGAGAGCTGTCA 300
Qy 301 GTCAAGAGCTGAGGCTGATGATGTAATGCTGCTGAGAGAGAGAGAGAGAG 360
Db 301 GTCAAGAGCTGAGGCTGATGATGTAATGCTGCTGAGAGAGAGAGAGAGAG 360
Qy 361 ATGAGAACATTTAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATGAGAACATTTAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 AAGCTGAACCACTGTAAGTGGAGTCTGCACTGCTGCTGAGAGAGAGAGAG 480
Db 421 AAGCTGAACCACTGTAAGTGGAGTCTGCACTGCTGCTGAGAGAGAGAGAG 480
Qy 481 AACTTTGAGCTTTCTCCAAAAA 509
Db 481 AACTTTGAGCTTTCTCCAAAAA 509

RESULT 3
US-10-051-835-11
Sequence 11, Application US/10051835
GENERAL INFORMATION:
APPLICANT: Jones, David A.
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS
FILE REFERENCE: PA-0044 US
CURRENT APPLICATION NUMBER: US/10/051,835
CURRENT FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PERL Program
SEQ ID NO: 11
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No: 064516CB1
US-10-051-835-11

Query Match 100.0%; Score 509; DB 44; Length 509;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

241 TCAGGGGTGAGCTGAGCTCAATGCTGCTGAGAGAGTATCTCCAGAGAGCTGTCA 300
Db 241 TCAGGGGTGAGCTGAGCTCAATGCTGCTGAGAGAGTATCTCCAGAGAGCTGTCA 300
Qy 301 GTCAAGAGCTGAGGCTGATGATGTAATGCTGCTGAGAGAGAGAGAGAGAG 360
Db 301 GTCAAGAGCTGAGGCTGATGATGTAATGCTGCTGAGAGAGAGAGAGAGAG 360
Qy 361 ATGAGAACATTTAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATGAGAACATTTAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 AAGCTGAACCACTGTAAGTGGAGTCTGCACTGCTGCTGAGAGAGAGAGAG 480
Db 421 AAGCTGAACCACTGTAAGTGGAGTCTGCACTGCTGCTGAGAGAGAGAGAG 480
Qy 481 AACTTTGAGCTTTCTCCAAAAA 509
Db 481 AACTTTGAGCTTTCTCCAAAAA 509

RESULT 4
US-10-093-766-35
Sequence 35, Application US/10093766
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REFERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO: 35
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No: 064516CB1
US-10-093-766-35

Query Match 100.0%; Score 509; DB 44; Length 509;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	100.0%	Score 509;	DB 73;	Length 509;
Best Local Similarity	100.0%	Pred. No. 2e-124;		
Matches 509;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;
Db	1	GAGTGTGAGGCTGTGAGGGTCCCTCTCTGCTGTCTGCACTTTTCTGTCCACTGTGA	60	
Db	1	GAGTGTGAGGCTGTGAGGGTCCCTCTCTGCTGTCTGCACTTTTCTGTCCACTGTGA	60	
Db	61	CGCACTGTGTGAATATGATTTGGCGAGAGATCAATATAGGCTTAGGCCGAGAG	120	
Db	61	CGCACTGTGTGAATATGATTTGGCGAGAGATCAATATAGGCTTAGGCCGAGAG	120	
Db	121	AAGTGTACCACTCCTGAGCTGATTTGGGCTATCTGTGAGCCCGGTGATGAGAGCTCA	180	
Db	121	AAGTGTACCACTCCTGAGCTGATTTGGGCTATCTGTGAGAGCCCGGTGATGAGAGCTCA	180	
Db	181	GCAAGAGAACCAACCAACTGAAGTCGAGATCTTGCACTGTGTCAAGAGAGAAAGAA	240	
Db	181	GCAAGAGAACCAACCAACTGAAGTCGAGATCTTGCACTGTGTCAAGAGAGAAAGAA	240	
Db	241	TGAGGTGAGCTGTGAGCTCAAGTGCCTGACCTGAAAGTGAATTTCCAGAGACTGTCA	300	
Db	241	TGAGGTGAGCTGTGAGCTCAAGTGCCTGACCTGAAAGTGAATTTCCAGAGACTGTCA	300	
Db	301	GTCAAGAAGTGGGGGTGATGTGAATAGTCTCTGATGACAGGGGAATTTCTGCCAA	360	
Db	301	GTCAAGAAGTGGGGGTGATGTGAATAGTCTCTGATGACAGGGGAATTTCTGCCAA	360	
Db	361	ATCAGACCAATTTAAATATCCGAGAGAGAGTGCAGGCAACCAACAGTTTAATGAGAC	420	
Db	361	ATCAGACCAATTTAAATATCCGAGAGAGAGTGCAGGCAACCAACAGTTTAATGAGAC	420	
Db	421	AGCTGAAACAACAACAATCTGTTTTTATCTAAGATTTGACTTAAAAATCAAAATA	480	
Db	421	AGCTGAAACAACAACAATCTGTTTTTATCTAAGATTTGACTTAAAAATCAAAATA	480	
Db	481	AACCTTGACGCTTCTCCAAAAAAA 509		

```

Oy      1 GAGTTGTAGAGGTGTGAAGGGTCGCGTTCCTGCTCTCGAAGCTTTTCTGTCGCCACATGAGA 60
Db      1 GAGTTGTAGAGGTGTGAAGGGTCGCGTTCCTGCTCTCTCGAAGCTTTTCTGTCGCCACATGAGA 60
Oy      61 CGCAGCTGTGTGAATATGATTTTGGCGAGAAAGTCAACATATAGGCTTAGGCTCGAGAG 120
Db      61 CGCAGCTGTGTGAATATGATTTTGGCGAGAAAGTCAACATATAGGCTTAGGCTCGAGAG 120
Oy      121 AAGTGTACCACTCCTGAGACTGATTGGGCTATAGCTGAGAGCCCGTGTATGAGAGCCTCA 180
Db      121 AAGTGTACCACTCCTGAGACTGATTGGGCTATAGCTGAGAGCCCGTGTATGAGAGCCTCA 180
Oy      181 GCAGAGGAGAACCAACACCTGAAAGTCGGGATCTTGCACTCTGTCAAGAGAGAGAAAGAA 240
Db      181 GCAGAGGAGAACCAACACCTGAAAGTCGGGATCTTGCACTCTGTCAAGAGAGAGAAAGAA 240
Oy      241 TCAGGGTGCAGCTGAGACTCAAGTSCCTGACCTGAGACCTGAAAGCTGATCTCCAGAGCTGTCTCA 300
Db      241 TCAGGGTGCAGCTGAGACTCAAGTSCCTGACCTGAGAGCTGATCTCCAGAGCTGTCTCA 300
Oy      301 GTCAAAAGATCGGGGGTGAATGTGGAAATGATCTGATGACCAAGGGGAAAGTTCTGCCAAA 360
Db      301 GTCAAAAGATCGGGGGTGAATGTGGAAATGATCTGATGACCAAGGGGAAAGTTCTGCCAAA 360
Oy      361 ATCAGAAACAATTTAAATGTCGAAAGAGAGTGCAGAGCAACACAGGTTTAAATGAAGAC 420
Db      361 ATCAGAAACAATTTAAATGTCGAAAGAGAGTGCAGAGCAACACAGGTTTAAATGAAGAC 420
Oy      421 AAGCTGAACACACAAAACGTGTTTATCTTAAGATATTGAATTTAAATATGAAATA 480
Db      421 AAGCTGAACACACAAAACGTGTTTATCTTAAGATATTGAATTTAAATATGAAATA 480
Oy      481 AACTTTGACAGCTTCTCCAAAAAATA 509
Db      481 AACTTTGACAGCTTCTCCAAAAAATA 509

RESULT 7
US-60-253-425-7
; SEQUENCE 7, Application US/60253425
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: CDNA5 CO-EXPRESSED WITH PLACENTAL STEROID SYNTHESIS GENES
; FILE REFERENCE: PB-0016 P
; CURRENT APPLICATION NUMBER: US/60/253,425

```

Sequence Alignment between

page 1 of 2

or US Pub. No.
2002/0137081)

Query Match	100.0%;	Score 2484;	DB 43;	Length 2484;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2484;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	GTATTATCTTGATATATACCATTAACAGTTACACTAAATTAATTAATTAGGAATTGAAT	60		
1	GTTTATCTTGATATTAACCATTAACAGTTACACTAAATTAATTAATTAGGAATTGAAT	60		
61	TGTTAGTTAATTGGCTTTATATTAATTATGTTTACGATTAATGTTGTCMAAGATCAATC	120		
61	TGTTAGTTAATTGGCTTTATATTAATTATGTTTACGATTAATGTTGTCMAAGATCAATC	120		
121	TACAAATAATAGTATAGTCAAGAAGATCTATCTTCCTCTCGGCCCTCAATAATATTC	180		
121	TACAAAATAATAGTATAGTCAAGAAGATCTATCTTCCTCTCGGCCCTCAATAATATTC	180		
181	TCCCTCTTCCCATTTAGTAACCATATATAAATTTATATTTACTTGCTTTAAATAATGT	240		
181	TCCCTCTTCCCATTTAGTAACCATATATAAATTTATATTTACTTGCTTTAAATAATGT	240		
241	AACAAAGTACATATAAATTGCTGCTACTCCCTCTTAGAGAAGTGTAGAAAATCTATGT	300		
241	AACAAAGTACATATAAATTGCTGCTACTCCCTCTTAGAGAAGTGTAGAAAATCTATGT	300		
301	TATATGACTTATCAGACATTGTTTAACTGACATGCAATTTTCTGCTACAAATGTTCCA	360		
301	TATATGACTTATCAGACATTGTTTAACTGACATGCAATTTTCTGCTACAAATGTTCCA	360		
361	GCAAGTATATATCTTGGATATATCACTTTTGCAATTTTGTGCAATATCATGTGGAGACA	420		
361	GCAAGTATATATCTTGGATATATCACTTTTGCAATTTTGTGCAATATCATGTGGAGACA	420		
421	TTCCCAACAGAGAGTGTATGATTAAGATTAAGTCACTTCACTTGGACCCCTTCCCTC	480		
421	TTCCCAACAGAGAGTGTATGATTAAGATTAAGTCACTTCACTTGGACCCCTTCCCTC	480		
481	CTTGGGCTCTGCTTGATGATGATACGACTTTTCTTGTAATGCTCTTACTTCCATCTGTGG	540		
481	CTTGGGCTCTGCTTGATGATGATACGACTTTTCTTGTAATGCTCTTACTTCCATCTGTGG	540		
541	GCAAGTGGCCCTCTTATCTTAGAACAACCTTTCACGCAATTCCTTAATCTCTTTAGCAACT	600		
541	GCAAGTGGCCCTCTTATCTTAGAACAACCTTTCACGCAATTCCTTAATCTCTTTAGCAACT	600		
601	CACCTCTGCTATTTTATGCTCTCAAGATTAACATGTCCTTTCTCAACAAGGCTTACTGTAC	660		
601	CACCTCTGCTATTTTATGCTCTCAAGATTAACATGTCCTTTCTCAACAAGGCTTACTGTAC	660		

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

21 CCTCATCTATTAGAGACTTTTCGTGTTTGTACCACTTTGATTCACCTTGCACA

781 GGATCATTGCTGCTCATAAATTTTGTGAATTAATATCTTGCTTATGTC

761 GGTCATAGTTGTGCTCATAATATTTTGAATTATATCTTGGTTATGTC

041ACAG11AA1CCAGGAATCAATCCAAATAAATCAATGACACAAATGATTC

901 GCTGAAGCACGAATTCATGTGTGGCATTGTATTGATGCGCAGCTCTATTCA

901 GCTGAGGACAGATTCATTGTGTGGCATTGTGATTGATGCCAGCTCATTCAT

[illegible]

Db	2101	GTGGTCGAATATTCCTCTCCCTCGGTGGCTTCTCTGATTAATCCACTAGGAATTT	2160
Qy	2161	TTGTGTTTCTTTTCTCAGGGAAATCTAAGGAGAAATTAACACTGTGCAAGGAAAA	2220
Db	2161	TTGTGTTTCTTTTCTCAGGGAAATTAAGGAGAAATTAACACTGTGCAAGGAAAA	2220
Qy	2221	AATAGATATGTGAAAGTTCACGTAAATTTCTCATCATCAGAGAGATTAAATTCAGAA	2280
Db	2221	AATAGATATGTGAAAGTTCACGTAAATTTCTCATCATCAGAGAGATTAAATTCAGAA	2280
Qy	2281	AGGAGAAAAACACAGCCAAAGAGAGATATCTAAAGACCAAGGATGTGTTTAATATGT	2340
Db	2281	AGGAGAAAAACACAGCCAAAGAGAGATATCTAAAGACCAAGGATGTGTTTAATATGT	2340
Qy	2341	CTAGGATGAAGAAATGCTAGAAACATGTGTGTCTGTAAATTAATCTAGAAATTAACATAT	2400
Db	2341	CTAGGATGAAGAAATGCTAGAAACATGTGTGTCTGTAAATTAATCTAGAAATTAACATAT	2400
Qy	2401	TTAAGTCATTAATGTGAAAATAATATATATATTTTCTTGGATTATGTCTGTATCTGGA	2460
Db	2401	TTAAGTCATTAATGTGAAAATAATATATATATTTTCTTGGATTATGTCTGTATCTGGA	2460
Qy	2461	AAAAATAAATTTCTTAATAAACTC	2484
Db	2461	AAAAATAAATTTCTTAATAAACTC	2484

~~SEA~~ ID no: 197 of 10/084, 817

Page 1 of 3

OY	2101	TGCAATGAAGTAACTGTGGTTGTTTCATCTCATGAAACCTTGATGCATGCGCTTTG	216
DB	2101	TGCAATGAAGTAACTGTGGTTGTTTCATCTCATGAAACCTTGATGCATGCGCTTTG	216
OY	2161	TATGCAATAATTGGTGGCAATATGATGTCATTCACCTTGATTAATTAATTTGG	222
DB	2161	TATGCAATAATTGGTGGCAATATGATGTCATTCACCTTGATTAATTAATTTGG	222
OY	2221	TTGTATTTAATATATATATACCTGTACAGCTTCAGTGTGCTTGAACATTTTAAACAT	228
DB	2221	TTGTATTTAATATATATATACCTGTACAGCTTCAGTGTGCTTGAACATTTTAAACAT	228
OY	2281	TTTTTGACATATTTTACTGTAAAATATTTTAAATGAAATTTAAATTAACATTTGATGT	234
DB	2281	TTTTTGACATATATTTACTGTAAAAATATTTTAAATGAAATTTAAATTAACATTTGATGT	234
OY	2341	TTACAT 2346	
DB	2341	TTACAT 2346	

RESULT 2
US-10-084-817-197
; Sequence 197, Application US/1008481.7
; GENERAL INFORMATION:
APPLICANT: Susan Stuart
APPLICANT: Ued G. Nuchtern
APPLICANT: Sharon E. Plom
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
PRIORITY FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIORITY FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 197
LENGTH: 2346
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 200578.1
US-10-084-817-197

Query Match 100.0%; Score 2346; DB 44; Length 2346;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2346; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY	1	GCCAGAGGGGAAAAAAAAAGATGATGCAAGGATATCTCTTTTGCAGTGGTCACTGATATTT	60
DB	1	GCCAGAGGGGAAAAAAAAAGATGATGCAAGGATATCTCTTTTGCAGTGGTCACTGATATTT	60
OY	61	GAGTACCTTGTGTGACAGGGGATATTTACAGATCTGTGGGAAAACTATTAAGCCTT	120
DB	61	GAGTACCTTGTGTGACAGGGGATATTTACAGATCTGTGGGAAAACTATTAAGCCTT	120
OY	121	TGCATGTTTAAGCTGTATTAATTTGTGGGTGTGAGTGTCTGACCTTAATGTGATAT	180
DB	121	TGCATGTTTAAGCTGTATTAATTTGTGGGTGTGAGTGTCTGACCTTAATGTGATAT	180
OY	181	AAAAATTGACATCAAAATTTTCCATCACTAACCTTATTAATGCAATTTGGAAGCAC	240
DB	181	AAAAATTGACATCAAAATTTTCCATCACTAACCTTATTAATGCAATTTGGAAGCAC	240
OY	241	AATCATATCACACTGGGAGGCCAATGCAATGTGGTTACCTGTCTCAGTTGAACTGTCT	300
DB	241	AATCATATCACACTGGGAGGCCAATGCAATGTGGTTACCTGTCTCAGTTGAACTGTCT	300
OY	301	TATTTCAAACAATTTCTGAATTAATTTTTCCTAGAAATTTCCCTTCAATCCAAGTACA	360
DB	301	TATTTCAAACAATTTCTGAATTAATTTTTCCTAGAAATTTCCCTTCAATCCAAGTACA	360

QY	1441	CAA	CAAGTGGAGTCCATTGAGCCAGGCGGAAGCTGTGGAACTCAGGTAACTCCCTTGAAG	1500
Db	1441	CAC	ACAGTGGAGTCCATTGAGCCAGGCGGAAGCTGTGGAACTCAGGTAACTCCCTTGAAG	1500
QY	1501	GAT	ATGCTGGACCCCATCTCTTGTGATCTGTGCTTAAACTGTAAATTATATACACAGCTAAA	1560
Db	1501	GAT	ATGCTGGACCCCATCTCTTGTGATCTGTGCTTAAACTGTAAATTATATACACAGCTAAA	1560
QY	1561	TCC	CTTACCTTGAAATCCAGGAATGCAATAGTAATGACCTGTATACCAATCCCGAAATTTCAAG	1620
Db	1561	TCC	CTTACCTTGAAATCCAGGAATGCAATAGTAATGACCTGTATACCAATCCCGAAATTTCAAG	1620
QY	1621	GGA	TCGTGGGTTGGCTCTGATATGTAACCAACAAGAACAGAGAGATCCAGCTGAAAAA	1680
Db	1621	GGA	TCGTGGGTTGGCTCTGATATGTAACCAACAAGAACAGAGAGATCCAGCTGAAAAA	1680
QY	1681	GAG	ATGCCCAATCCCAATATCTCTAATCACTGCGTCCCACTCAAGAGAGTTCTTCACTCTG	1740
Db	1681	GAG	ATGCCCAATCCCAATATCTCTAATCACTGCGTCCCACTCAAGAGAGTTCTTCACTCTG	1740
QY	1741	GCA	CTGTGATCATGAAACTTAGTAGAGGGGGATGTGTGTAATTTATACAAATTTAATACA	1800
Db	1741	GCA	CTGTGATCATGAAACTTAGTAGAGGGGGATGTGTGTAATTTATACAAATTTAATACA	1800
QY	1801	ATG	CTTACCTGATATATAATTTCTTAAAGGCAAACTCGACTTTATTTCTGTCATCCACAT	1860
Db	1801	ATG	CTTACCTGATATATAATTTCTTAAAGGCAAACTCGACTTTATTTCTGTCATCCACAT	1860
QY	1861	TCC	CAATCATATTAGAACTAAGATATTATTCATGAGAAATATAATGGTGCAGAGAGACTT	1920
Db	1861	TCC	CAATCATATTAGAACTAAGATATTATTCATGAGAAATATAATGGTGCAGAGAGACTT	1920
QY	1921	TCA	TCTGTGGATGCGCTGTGTTCTTAGAGGTCCCTAGACCTGAAGCCCTGCACAGCAATGTG	1980
Db	1921	TCA	TCTGTGTGGATGCGCTGTGTTCTTAGAGGTCCCTAGACCTGAAGCCCTGCACAGCAATGTG	1980
QY	1981	ATA	TGTGAATAATGAATGATCTCTCTATACCTAAATGATTCCTCTGGGGAGAGTTCTG	2040
Db	1981	ATA	TGTGAATAATGAATGATCTCTCTATACCTAAATGATTCCTCTGGGGAGAGTTCTG	2040
QY	2041	GTA	CTGCATCACTACATGCCACAGATGCTTTATATGGGCTAATTTGTGTAACTAATGTATAGA	2100
Db	2041	GTA	CTGCATGCATCACTACATGCCACAGATGCTTTATATGGGCTAATTTGTGTAACTAATGTATAGA	2100
QY	2101	TGC	TATGAAGTAAAGTGTGTTGTTTCATCTTATGAAACCTCTGATGCAATGTGCTTTTG	2160
Db	2101	TGC	TATGAAGTAAAGTGTGTTGTTTCATCTTATGAAACCTCTGATGCAATGTGCTTTTG	2160
QY	2161	TAT	GGAATTAATTTGGTGCATATATGATGTCATTTCACTTTGCACTTGAATTTGAATTTTGG	2220
Db	2161	TAT	GGAATTAATTTGGTGCATATATGATGTCATTTCACTTTGCACTTGAATTTGAATTTTGG	2220
QY	2221	TGT	ATTTAATATGATATATACCTGTGACGGCTTCACTAGTGTGCTCAACATTTTATACCAT	2280
Db	2221	TGT	ATTTAATTTAATATGATATATACCTGTGACGGCTTCACTAGTGTGCTCAACATTTTATACCAT	2280
QY	2281	TTT	TGTACATATTTTACTGAAATAATTTTAAATGAGAAATTTAATATAACATTTGATAGT	2340
Db	2281	TTT	TGTGTACATATTTTACTGAAATAATTTTAAATGAGAAATTTAATATAACATTTGATAGT	2340
QY	2341	TTA	CAAT 2346	
Db	2341	TTA	CAAT 2346	

~~CURRENT APPLICATION NUMBER:~~ US/10/116,802

Sequence Alignment between
SEQ ID NO: 126 of 09/974, 298 (or US Pub.
and SEQ ID NO: 11
NO. 2007015263)

OTHER INFORMATION: Inocyte ID No: 064516C81
US-09-974-298-126

Query Match 100.0%; Score 509; DB 41; Length 509;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Result No.	Score	Query Match	Length	ID	Description
1	509	100.0	509	41	Sequence 126, App
2	509	100.0	509	42	Sequence 7, Appl
3	509	100.0	509	44	Sequence 11, Appl
4	509	100.0	509	44	Sequence 35, Appl
5	509	100.0	509	73	Sequence 1343, A
6	509	100.0	509	80	Sequence 126, Appl
7	509	100.0	509	82	Sequence 7, Appl
8	509	100.0	509	84	Sequence 11, Appl
9	509	100.0	509	84	Sequence 35, Appl
10	505.8	99.4	871	1	Sequence 7668, Ap
11	505.8	99.4	871	54	Sequence 7668, Ap
12	504.6	99.1	517	34	Sequence 12130, A
13	504.6	99.1	517	75	Sequence 12130, A
14	504.2	99.1	517	1	Sequence 38, Appl
15	499	98.0	547	1	Sequence 3717, Ap
16	499	98.0	547	54	Sequence 3717, Ap
17	483.4	95.0	659	20	Sequence 947, App
18	483.4	95.0	659	20	Sequence 947, App
19	483.4	95.0	659	43	Sequence 634, App
20	483.4	95.0	659	45	Sequence 634, App
21	483.4	95.0	659	48	Sequence 947, App
22	483.4	95.0	659	48	Sequence 947, App
23	480.6	94.4	532	20	Sequence 441, App
24	480.6	94.4	532	20	Sequence 4519, App
25	480.6	94.4	532	20	Sequence 7457, App
26	480.6	94.4	532	48	Sequence 4519, App
27	480.6	94.4	532	48	Sequence 4519, App
28	477.8	89.9	550	44	Sequence 109, App
29	456	89.6	513	44	Sequence 111, App
30	452.8	89.0	513	44	Sequence 6619, App
31	452.8	89.0	513	75	Sequence 6619, App
32	452.8	89.0	513	75	Sequence 5956, App
33	421.4	82.8	503	1	Sequence 5286, App
34	421.4	82.8	503	1	Sequence 5286, App
35	412.6	81.1	484	75	Sequence 6618, App
36	392.6	75.2	645	16	Sequence 6290, App
37	392.6	75.2	645	16	Sequence 13741, A
38	392.6	75.2	645	18	Sequence 13741, A
39	392.6	75.2	645	36	Sequence 13741, A
40	382.6	75.2	645	36	Sequence 13741, A
41	361.8	71.1	426	34	Sequence 30733, A
42	361.8	71.1	426	75	Sequence 30733, A
43	360.4	70.8	362	20	Sequence 7947, App
44	360.4	70.8	362	20	Sequence 7947, App
45	359.8	70.7	427	46	Sequence 4606, App

ALIGNMENTS

RESULT 1
US-09-974-298-126
Sequence 126, Application US/09974298
GENERAL INFORMATION:
APPLICANT: Chen, Huel-Mel
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974, 298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238, 331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 126
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

Wed

Query Match	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	509	41	509	509	0	0	0	0
2	509	42	509	509	0	0	0	0
3	509	44	509	509	0	0	0	0
4	509	44	509	509	0	0	0	0
5	509	73	509	509	0	0	0	0
6	509	80	509	509	0	0	0	0
7	509	82	509	509	0	0	0	0
8	509	84	509	509	0	0	0	0
9	509	84	509	509	0	0	0	0
10	505.8	99.4	871	1	0	0	0	0
11	505.8	99.4	871	54	0	0	0	0
12	504.6	99.1	517	34	0	0	0	0
13	504.6	99.1	517	75	0	0	0	0
14	504.2	99.1	517	1	0	0	0	0
15	499	98.0	547	1	0	0	0	0
16	499	98.0	547	54	0	0	0	0
17	483.4	95.0	659	20	0	0	0	0
18	483.4	95.0	659	20	0	0	0	0
19	483.4	95.0	659	43	0	0	0	0
20	483.4	95.0	659	45	0	0	0	0
21	483.4	95.0	659	48	0	0	0	0
22	483.4	95.0	659	48	0	0	0	0
23	480.6	94.4	532	20	0	0	0	0
24	480.6	94.4	532	20	0	0	0	0
25	480.6	94.4	532	20	0	0	0	0
26	480.6	94.4	532	48	0	0	0	0
27	480.6	94.4	532	48	0	0	0	0
28	477.8	89.9	550	44	0	0	0	0
29	456	89.6	513	44	0	0	0	0
30	452.8	89.0	513	44	0	0	0	0
31	452.8	89.0	513	75	0	0	0	0
32	452.8	89.0	513	75	0	0	0	0
33	421.4	82.8	503	1	0	0	0	0
34	421.4	82.8	503	1	0	0	0	0
35	412.6	81.1	484	75	0	0	0	0
36	392.6	75.2	645	16	0	0	0	0
37	392.6	75.2	645	16	0	0	0	0
38	392.6	75.2	645	18	0	0	0	0
39	392.6	75.2	645	36	0	0	0	0
40	382.6	75.2	645	36	0	0	0	0
41	361.8	71.1	426	34	0	0	0	0
42	361.8	71.1	426	75	0	0	0	0
43	360.4	70.8	362	20	0	0	0	0
44	360.4	70.8	362	20	0	0	0	0
45	359.8	70.7	427	46	0	0	0	0

RESULT 2
US-09-974-298-126
Sequence 126, Application US/09974298
GENERAL INFORMATION:
APPLICANT: Wong, Sophia M-Ling
TITLE OF INVENTION: CDNA CO-EXPRESSED WITH PLACENTAL STEROID SYNTHESIS GENES
FILE REFERENCE: PB-0016 US
CURRENT APPLICATION NUMBER: US/09/974, 298
CURRENT FILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Inocyte ID No: 253708
US-09-974-298-126

Query Match	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	509	41	509	509	0	0	0	0
2	509	42	509	509	0	0	0	0
3	509	44	509	509	0	0	0	0
4	509	44	509	509	0	0	0	0
5	509	73	509	509	0	0	0	0
6	509	80	509	509	0	0	0	0
7	509	82	509	509	0	0	0	0
8	509	84	509	509	0	0	0	0
9	509	84	509	509	0	0	0	0
10	505.8	99.4	871	1	0	0	0	0
11	505.8	99.4	871	54	0	0	0	0
12	504.6	99.1	517	34	0	0	0	0
13	504.6	99.1	517	75	0	0	0	0
14	504.2	99.1	517	1	0	0	0	0
15	499	98.0	547	1	0	0	0	0
16	499	98.0	547	54	0	0	0	0
17	483.4	95.0	659	20	0	0	0	0
18	483.4	95.0	659	20	0	0	0	0
19	483.4	95.0	659	43	0	0	0	0
20	483.4	95.0	659	45	0	0	0	0
21	483.4	95.0	659	48	0	0	0	0
22	483.4	95.0	659	48	0	0	0	0
23	480.6	94.4	532	20	0	0	0	0
24	480.6	94.4	532	20	0	0	0	0
25	480.6	94.4	532	20	0	0	0	0
26	480.6	94.4	532	48	0	0	0	0
27	480.6	94.4	532	48	0	0	0	0
28	477.8	89.9	550	44	0	0	0	0
29	456	89.6	513	44	0	0	0	0
30	452.8	89.0	513	44	0	0	0	0
31	452.8	89.0	513	75	0	0	0	0
32	452.8	89.0	513	75	0	0	0	0
33	421.4	82.8	503	1	0	0	0	0
34	421.4	82.8	503	1	0	0	0	0
35	412.6	81.1	484	75	0	0	0	0
36	392.6	75.2	645	16	0	0	0	0
37	392.6	75.2	645	16	0	0	0	0
38	392.6	75.2	645	18	0	0	0	0
39	392.6	75.2	645	36	0	0	0	0
40	382.6	75.2	645	36	0	0	0	0
41	361.8	71.1	426	34	0	0	0	0
42	361.8	71.1	426	75	0	0	0	0
43	360.4	70.8	362	20	0	0	0	0
44	360.4	70.8	362	20	0	0	0	0
45	359.8	70.7	427	46	0	0	0	0